

DRAFTU.S. Application No. 09/965,553
Attorney Ref. No.: 08411-030002
05/12/03**PROPOSED NEW CLAIM****BEST AVAILABLE COPY**

XX. The isolated nucleic acid of claim 56,

wherein said pol gene comprises:

at least a portion of a plant integrase sequence, wherein said integrase sequence comprises a nucleic acid sequence selected from the group consisting of:

- (a) a nucleic acid having at least 70% identity to the sequence shown in SEQ ID NO:9, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (b) a nucleic acid having the sequence shown in SEQ ID NO:9;
- (c) a nucleic acid that encodes an amino acid having at least 75% identity to the sequence shown in SEQ ID NO:10, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (d) a nucleic acid that encodes an amino acid having the sequence shown in SEQ ID NO:10; and
- (e) a nucleic acid having a sequence fully complementary to (a), (b), (c), or (d);

at least a portion of a plant reverse transcriptase sequence, wherein said reverse transcriptase sequence comprises a nucleic acid sequence selected from the group consisting of:

- (f) a nucleic acid having at least 70% identity to the sequence shown in SEQ ID NO:11, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (g) a nucleic acid having the sequence shown in SEQ ID NO:11;
- (h) a nucleic acid that encodes an amino acid having at least 79% identity to the sequence shown in SEQ ID NO:12, wherein said identity can be determined using the DNAsis computer program and default parameters;
- (i) a nucleic acid that encodes an amino acid having the sequence shown in SEQ ID NO:12; and

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(j) a nucleic acid having a sequence fully complementary to
(f), (g), (h), or (i); and

at least a portion of a plant RNaseH sequence, wherein said
RNaseH sequence comprises a nucleic acid sequence selected from the group consisting
of:

(k) a nucleic acid sequence having at least 70% identity to
the sequence shown in SEQ ID NO:15, wherein said identity can be determined using the
DNAsis computer program and default parameters;

(l) a nucleic acid having the sequence shown in SEQ ID
NO:15;

(m) a nucleic acid sequence that encodes an amino acid
sequence having at least 90% identity to the sequence shown in SEQ ID NO:16, wherein
said identity can be determined using the DNAsis computer program and default
parameters;

(n) a nucleic acid sequence that encodes an amino acid
having the sequence shown in SEQ ID NO:16; and

(o) a nucleic acid having a sequence fully complementary
to (k), (l), (m), or (n);

wherein said env gene comprises at least a portion of a plant envelope
sequence, wherein said envelope sequence comprises a nucleic acid sequence selected
from the group consisting of:

(p) a nucleic acid having at least 50% identity to the sequence
shown in SEQ ID NO:5, wherein said identity can be determined using the DNAsis
computer program and default parameters;

(q) a nucleic acid having the sequence shown in SEQ ID NO:5;

(r) a nucleic acid that encodes an amino acid having at least 30%
identity to the sequence shown in SEQ ID NO:6, wherein said identity can be determined
using the DNAsis computer program and default parameters;

(s) a nucleic acid that encodes an amino acid having the sequence
shown in SEQ ID NO:6; and

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(t) a nucleic acid having a sequence fully complementary to (p),
(q), (r), or (s);

and wherein said isolated nucleic acid further comprises:

a nucleic acid having the sequence shown in SEQ ID NO:4; and

a nucleic acid comprising the sequence shown in SEQ ID NO:3 or
the complement of the sequence shown in SEQ ID NO:3, wherein said nucleic acid
encodes a plant retroviral polypurine tract.

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